Kubelik

#5

RAW SEQUENCE LISTING   DATE: 08/02/2001
PATENT APPLICATION: US/09/597,840   TIME: 10:40:35

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

SEQUENCE LISTING

```
 4 (1) GENERAL INFORMATION:
 6       (i) APPLICANT: Qiu, Dewen
 7                      Wei, Zhong-Min
 8                      Beer, Steven V.
10      (ii) TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
12     (iii) NUMBER OF SEQUENCES: 10
14      (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
16           (B) STREET: Clinton Square, P.O. Box 1051
17           (C) CITY: Rochester
18           (D) STATE: New York
19           (E) COUNTRY: U.S.A.
20           (F) ZIP: 14603
22       (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Floppy disk
24           (B) COMPUTER: IBM PC compatible
25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28      (vi) CURRENT APPLICATION DATA:
29           (A) APPLICATION NUMBER: US/09/597,840
30           (B) FILING DATE: 20-Jun-2000
31           (C) CLASSIFICATION:
33     (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: 09/013,587
35           (B) FILING DATE:
37    (viii) ATTORNEY/AGENT INFORMATION:
38           (A) NAME: Goldman, Michael L.
39           (B) REGISTRATION NUMBER: 30,727
40           (C) REFERENCE/DOCKET NUMBER: 19603/1501
42      (ix) TELECOMMUNICATION INFORMATION:
43           (A) TELEPHONE: (716) 263-1304
44           (B) TELEFAX: (716) 263-1600
47 (2) INFORMATION FOR SEQ ID NO: 1:
49       (i) SEQUENCE CHARACTERISTICS:
50           (A) LENGTH: 338 amino acids
51           (B) TYPE: amino acid
52           (C) STRANDEDNESS:
53           (D) TOPOLOGY: linear
55      (ii) MOLECULE TYPE: protein
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62           Met Gln Ile Thr Ile Lys Ala His Ile Gly Gly Asp Leu Gly Val Ser
63           1               5                   10                  15
65           Gly Leu Gly Ala Gln Gly Leu Lys Gly Leu Asn Ser Ala Ala Ser Ser
66                       20                  25                  30
68           Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr
69                       35                  40                  45
```

C--> 29
C--> 30

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71      Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu
72          50                  55                  60
74      Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser
75          65                  70                  75                  80
77      Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys
78                          85                  90                  95
80      Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp
81                      100                 105                 110
83      Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln
84                  115                 120                 125
86      Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met
87          130                 135                 140
89      Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly
90          145                 150                 155                 160
92      Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly
93                      165                 170                 175
95      Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu
96                      180                 185                 190
98      Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala
99                  195                 200                 205
101     Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val
102         210                 215                 220
104     Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp
105     225                 230                 235                 240
107     Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp
108                     245                 250                 255
110     Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
111                     260                 265                 270
113     Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
114                 275                 280                 285
116     Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
117         290                 295                 300
119     Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
120     305                 310                 315                 320
122     Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala
123                 325                 330                 335
125     Asn Ala
128 (2) INFORMATION FOR SEQ ID NO: 2:
130     (i) SEQUENCE CHARACTERISTICS:
131         (A) LENGTH: 2141 base pairs
132         (B) TYPE: nucleic acid
133         (C) STRANDEDNESS: single
134         (D) TOPOLOGY: linear
136     (ii) MOLECULE TYPE: DNA (genomic)
141     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
143 CGATTTTACC CGGGTGAACG TGCTATGACC GACAGCATCA CGGTATTCGA CACCGTTACG      60
145 GCGTTTATGG CCGCGATGAA CCGGCATCAG GCGGCGCGCT GGTCGCCGCA ATCCGGCGTC     120
147 GATCTGGTAT TTCAGTTTGG GGACACCGGG CGTGAACTCA TGATGCAGAT TCAGCCGGGG     180
149 CAGCAATATC CCGGCATGTT GCGCACGCTG CTCGCTCGTC GTTATCAGCA GGCGGCAGAG     240
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/597,840**

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Output Set: **N:\CRF3\08022001\I597840.raw**

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151 TGCGATGGCT GCCATCTGTG CCTGAACGGC AGCGATGTAT TGATCCTCTG GTGGCCGCTG    300
153 CCGTCGGATC CCGGCAGTTA TCCGCAGGTG ATCGAACGTT TGTTTGAACT GGCGGGAATG    360
155 ACGTTGCCGT CGCTATCCAT AGCACCGACG GCGCGTCCGC AGACAGGGAA CGGACGCGCC    420
157 CGATCATTAA GATAAAGGCG GCTTTTTTTA TTGCAAAACG GTAACGGTGA GGAACCGTTT    480
159 CACCGTCGGC GTCACTCAGT AACAAGTATC CATCATGATG CCTACATCGG GATCGGCGTG    540
161 GGCATCCGTT GCAGATACTT TTGCGAACAC CTGACATGAA TGAGGAAACG AAATTATGCA    600
163 AATTACGATC AAAGCGCACA TCGGCGGTGA TTTGGGCGTC TCCGGTCTGG GGCTGGGTGC    660
165 TCAGGGACTG AAAGGACTGA ATTCCGCGGC TTCATCGCTG GGTTCCAGCG TGGATAAACT    720
167 GAGCAGCACC ATCGATAAGT TGACCTCCGC GCTGACTTCG ATGATGTTTG GCGGCGCGCT    780
169 GGCGCAGGGG CTGGGCGCCA GCTCGAAGGG GCTGGGGATG AGCAATCAAC TGGGCCAGTC    840
171 TTTCGGCAAT GGCGCGCAGG GTGCGAGCAA CCTGCTATCC GTACCGAAAT CCGGCGGCGA    900
173 TGCGTTGTCA AAAATGTTTG ATAAAGCGCT GGACGATCTG CTGGGTCATG ACACCGTGAC    960
175 CAAGCTGACT AACCAGAGCA ACCAACTGGC TAATTCAATG CTGAACGCCA GCCAGATGAC   1020
177 CCAGGGTAAT ATGAATGCGT TCGGCAGCGG TGTGAACAAC GCACTGTCGT CCATTCTCGG   1080
179 CAACGGTCTC GGCCAGTCGA TGAGTGGCTT CTCTCAGCCT TCTCTGGGGG CAGGCGGCTT   1140
181 GCAGGGCCTG AGCGGCGCGG GTGCATTCAA CCAGTTGGGT AATGCCATCG GCATGGGCGT   1200
183 GGGGCAGAAT GCTGCGCTGA GTGCGTTGAG TAACGTCAGC ACCCACGTAG ACGGTAACAA   1260
185 CCGCCACTTT GTAGATAAAG AAGATCGCGG CATGGCGAAA GAGATCGGCC AGTTTATGGA   1320
187 TCAGTATCCG GAAATATTCG GTAAACCGGA ATACCAGAAA GATGGCTGGA GTTCGCCGAA   1380
189 GACGGACGAC AAATCCTGGG CTAAAGCGCT GAGTAAACCG GATGATGACG GTATGACCGG   1440
191 CGCCAGCATG GACAAATTCC GTCAGGCGAT GGGTATGATC AAAAGCGCGG TGGCGGGTGA   1500
193 TACCGGCAAT ACCAACCTGA ACCTGCGTGG CGCGGGCGGT GCATCGCTGG GTATCGATGC   1560
195 GGCTGTCGTC GGCGATAAAA TAGCCAACAT GTCGCTGGGT AAGCTGGCCA ACGCCTGATA   1620
197 ATCTGTGCTG GCCTGATAAA GCGGAAACGA AAAAAGAGAC GGGGAAGCCT GTCTCTTTTC   1680
199 TTATTATGCG GTTTATGCGG TTACCTGGAC CGGTTAATCA TCGTCATCGA TCTGGTACAA   1740
201 ACGCACATTT TCCCGTTCAT TCGCGTCGTT ACGCGCCACA ATCGCGATGG CATCTTCCTC   1800
203 GTCGCTCAGA TTGCGCGGCT GATGGGGAAC GCCGGGTGGA ATATAGAGAA ACTCGCCGGC   1860
205 CAGATGGAGA CACGTCTGCG ATAAATCTGT GCCGTAACGT GTTTCTATCC GCCCCTTTAG   1920
207 CAGATAGATT GCGGTTTCGT AATCAACATG GTAATGCGGT TCCGCCTGTG CGCCGGCCGG   1980
209 GATCACCACA ATATTCATAG AAAGCTGTCT TGCACCTACC GTATCGCGGG AGATACCGAC   2040
211 AAAATAGGGC AGTTTTTGCG TGGTATCCGT GGGGTGTTCC GGCCTGACAA TCTTGAGTTG   2100
213 GTTCGTCATC ATCTTTCTCC ATCTGGGCGA CCTGATCGGT T                        2141
215 (2) INFORMATION FOR SEQ ID NO: 3:
217     (i) SEQUENCE CHARACTERISTICS:
218         (A) LENGTH: 403 amino acids
219         (B) TYPE: amino acid
220         (C) STRANDEDNESS:
221         (D) TOPOLOGY: linear
223     (ii) MOLECULE TYPE: protein
228     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
230     Met Ser Leu Asn Thr Ser Gly Leu Gly Ala Ser Thr Met Gln Ile Ser
231     1               5                   10                  15
233     Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln
234                     20                  25                  30
236     Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Gly Asn
237                 35                  40                  45
239     Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
240         50                  55                  60
242     Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
```

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Input Set : N:\Crf3\RULE60\09597840.txt
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```
243    65                   70                  75                    80
245    Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
246                   85                  90                   95
248    Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
249                  100                 105                  110
251    Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
252                  115                 120                  125
254    Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
255                  130                 135                  140
257    Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
258    145                 150                 155                  160
260    Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
261                  165                 170                  175
263    Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
264                  180                 185                  190
266    Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
267                  195                 200                  205
269    Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
270    210                 215                 220
272    Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
273    225                 230                 235                  240
275    Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
276                  245                 250                  255
278    Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln
279                  260                 265                  270
281    Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe
282                  275                 280                  285
284    Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met
285    290                 295                 300
287    Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro
288    305                 310                 315                  320
290    Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
291                  325                 330                  335
293    Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
294                  340                 345                  350
296    Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
297                  355                 360                  365
299    Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
300    370                 375                 380
302    Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu
303    385                 390                 395                  400
305    Gly Ala Ala
308 (2) INFORMATION FOR SEQ ID NO: 4:
310        (i) SEQUENCE CHARACTERISTICS:
311            (A) LENGTH: 1288 base pairs
312            (B) TYPE: nucleic acid
313            (C) STRANDEDNESS: single
314            (D) TOPOLOGY: linear
316        (ii) MOLECULE TYPE: DNA (genomic)
```

```
321    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
323 AAGCTTCGGC ATGGCACGTT TGACCGTTGG GTCGGCAGGG TACGTTTGAA TTATTCATAA     60
325 GAGGAATACG TTATGAGTCT GAATACAAGT GGGCTGGGAG CGTCAACGAT GCAAATTTCT    120
327 ATCGGCGGTG CGGGCGGAAA TAACGGGTTG CTGGGTACCA GTCGCCAGAA TGCTGGGTTG    180
329 GGTGGCAATT CTGCACTGGG GCTGGGCGGC GGTAATCAAA ATGATACCGT CAATCAGCTG    240
331 GCTGGCTTAC TCACCGGCAT GATGATGATG ATGAGCATGA TGGGCGGTGG TGGGCTGATG    300
333 GGCGGTGGCT TAGGCGGTGG CTTAGGTAAT GGCTTGGGTG GCTCAGGTGG CCTGGGCGAA    360
335 GGACTGTCGA ACGCGCTGAA CGATATGTTA GGCGGTTCGC TGAACACGCT GGGCTCGAAA    420
337 GGCGGCAACA ATACCACTTC AACAACAAAT TCCCCGCTGG ACCAGGCGCT GGGTATTAAC    480
339 TCAACGTCCC AAAACGACGA TTCCACCTCC GGCACAGATT CCACCTCAGA CTCCAGCGAC    540
341 CCGATGCAGC AGCTGCTGAA GATGTTCAGC GAGATAATGC AAAGCCTGTT TGGTGATGGG    600
343 CAAGATGGCA CCCAGGGCAG TTCCTCTGGG GGCAAGCAGC CGACCGAAGG CGAGCAGAAC    660
345 GCCTATAAAA AAGGAGTCAC TGATGCGCTG TCGGGCCTGA TGGGTAATGG TCTGAGCCAG    720
347 CTCCTTGGCA ACGGGGGACT GGGAGGTGGT CAGGGCGGTA ATGCTGGCAC GGGTCTTGAC    780
349 GGTTCGTCGC TGGGCGGCAA AGGGCTGCAA AACCTGAGCG GCCGGTGGA CTACCAGCAG     840
351 TTAGGTAACG CCGTGGGTAC CGGTATCGGT ATGAAAGCGG GCATTCAGGC GCTGAATGAT    900
353 ATCGGTACGC ACAGGCACAG TTCAACCCGT TCTTTCGTCA ATAAAGGCGA TCGGGCGATG    960
355 GCGAAGGAAA TCGGTCAGTT CATGGACCAG TATCCTGAGG TGTTTGGCAA GCCGCAGTAC   1020
357 CAGAAAGGCC CGGGTCAGGA GGTGAAAACC GATGACAAAT CATGGGCAAA AGCACTGAGC   1080
359 AAGCCAGATG ACGACGGAAT GACACCAGCC AGTATGGAGC AGTTCAACAA AGCCAAGGGC   1140
361 ATGATCAAAA GGCCCATGGC GGGTGATACC GGCAACGGCA ACCTGCAGGC ACGCGGTGCC   1200
363 GGTGGTTCTT CGCTGGGTAT TGATGCCATG ATGGCCGGTG ATGCCATTAA CAATATGGCA   1260
365 CTTGGCAAGC TGGGCGCGGC TTAAGCTT                                      1288
367 (2) INFORMATION FOR SEQ ID NO: 5:
369       (i) SEQUENCE CHARACTERISTICS:
370           (A) LENGTH: 341 amino acids
371           (B) TYPE: amino acid
372           (C) STRANDEDNESS:
373           (D) TOPOLOGY: linear
375      (ii) MOLECULE TYPE: protein
380      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
382       Met Gln Ser Leu Ser Leu Asn Ser Ser Ser Leu Gln Thr Pro Ala Met
383       1               5                   10                  15
385       Ala Leu Val Leu Val Arg Pro Glu Ala Glu Thr Thr Gly Ser Thr Ser
386                       20                  25                  30
388       Ser Lys Ala Leu Gln Glu Val Val Val Lys Leu Ala Glu Glu Leu Met
389                   35                  40                  45
391       Arg Asn Gly Gln Leu Asp Asp Ser Ser Pro Leu Gly Lys Leu Leu Ala
392               50                  55                  60
394       Lys Ser Met Ala Ala Asp Gly Lys Ala Gly Gly Gly Ile Glu Asp Val
395       65                  70                  75                  80
397       Ile Ala Ala Leu Asp Lys Leu Ile His Glu Lys Leu Gly Asp Asn Phe
398                       85                  90                  95
400       Gly Ala Ser Ala Asp Ser Ala Ser Gly Thr Gly Gln Gln Asp Leu Met
401                       100                 105                 110
403       Thr Gln Val Leu Asn Gly Leu Ala Lys Ser Met Leu Asp Asp Leu Leu
404                   115                 120                 125
406       Thr Lys Gln Asp Gly Gly Thr Ser Phe Ser Glu Asp Asp Met Pro Met
407               130                 135                 140
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VERIFICATION SUMMARY   DATE: 08/02/2001
PATENT APPLICATION: **US/09/597,840**   TIME: 10:40:36

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]